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Arabidopsis thalia
C albicans apoptos
Plant microsatelli
              Fusarium venenatum
Probe #20973 used
Aspergillus oryzae
S cerevisiae apopt
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colon ca		genome fra	#2137 used	e #2273		Plant microsatelli			Oligonucleotide D2		Oligonucleotide D1	Oligonucleotide D1	Human secreted pro			Oligonucleotide D2		Oligonucleotide D1		ovarian tum	#7117 u	#15406 use	Probe #11364 for q	Œ	#6692 for	Probe #22011 used	Probe #15887 for q	Human secreted pro		ısı	ys DNA fraq	used	Trichoderma reesei

ALIGNMENTS

Arabidopsis thaliana DNA fragment SEQ ID NO: 59811.

18-OCT-2000 (first entry)

AAC49069 standard; DNA; 637

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AAC49069;

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                                                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
        25-FEB-2000; 2000EP-0301439.
                                           06-SEP-2000
                                                                                                           Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                          AAC45801 standard;
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nilarity 62.7%;
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99US-0161404.
99US-0161405.
99US-0161359.
99US-0161361.
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99US-0140695

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99US-0141287

99US-0141287

99US-0142154

99US-0142803

99US-0142803
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RESULT 3
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nilarity 62.3%;
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             (first entry)
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                                                         DNA;
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                                                           638
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99US-0139456. 99US-0139456. 99US-0139458. 99US-0139459. 99US-0139460. 99US-0139461. 99US-0139463. 99US-013963. 99US-013963. 99US-0139763.	99US-0134941. 99US-0135124. 99US-013535. 99US-0135629. 99US-0136091. 99US-013692. 99US-013722. 99US-0137228. 99US-0137528. 99US-0137528. 99US-0137502. 99US-0137502. 99US-0137502. 99US-0137502. 99US-0137502. 99US-0137502.	99US-0130475 99US-0130077 99US-0130449 99US-0130510 99US-0130891 99US-0131449 99US-0132487 99US-0132485 99US-0132485 99US-0132486 99US-0132486 99US-0132487 99US-0132487 99US-0132487 99US-0132486 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0134256 99US-0134256	Arabidopsis thaliana DNA fragment SEQ ID NO: 7218. Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss. Arabidopsis thaliana. EP1033405-A2. 06-SEP-2000. 25-FEB-2000; 2000EP-0301439. 25-FEB-1999; 99US-0121825. 05-MAR-1999; 99US-0123548. 09-MAR-1999; 99US-0125788. 25-MAR-1999; 99US-0126783. 01-APR-1999; 99US-0126783. 01-APR-1999; 99US-0126784. 06-APR-1999; 99US-0128734.
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ies 120;
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99US-0128714
99US-0130449
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Best Local :
                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identitreatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaem and neurodegeneration. The present sequence is one of the C. albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in certain diseases -
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ttccaaagttgtatcgtcgtctagaagaaagcagaggaaagcatactttcaagcaccatc
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                                                                                                                                                                                                                                               sequences
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                                                                                                  Similarity
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Reekmans RJ;
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                                                                                                                                                                                                                                                  of the invention.
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                                                                                                                                                                                                    196 G;
                                                                                                                                                                                                      446 T; 0 other;
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                                             Sequences AAA31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant microsatellite sequence; core repeat sequence; detection;
DNA polymorphism; genome mapping; physical mapping; fingerprintly
variety identification; genetic variability evaluation; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant microsatellite markers and associated flanking detection of polymorphic genetic markers \dot{\boldsymbol{\cdot}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aggttctgaaggtaaagttaattctgtttatagattgaaatttgctattcaagttgataa
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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative expression of the same genes in one or more second filamentous funga
                                                                                                                                                                                                                                                                                                                                                             (NOVO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                             Moditoring differential expression of genes in filamentous uses fluorescence-labeled nucleic acids isolated from the c
                                                                                                           Claim 86;
                                                                                                                                                                                                                                                               WPI; 2000-594572/56.
                                                                                                                                                                                                                                                                                                                 Berka RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-1999;
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cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogeness, recombination, metabolic or catabolic pathway
                                                  engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.
     Sequence
     788
     B₽;
     186 A;
  246 C;
     181 G;
     175
T; 0 other;
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밁 QΥ 밁 Qy DЬ Ω Qy Вb Вb Qy Query Match Best Local Matches 173; 256 298 196 238 136 178 118 cgtcgtctagaagaaagcagaggaaagcatactttcaagcaccatcttctgtacgacgaa 177 76 Local Similarity aagttacaacgtgttatcgaaagaaatatcggatacatatcgagagagtgaccagagaaa cttcttctcgccgcaagagccgtgccgctcacttcaaggctccctctgaccagcgccgtg 135 agatcacctccgtgtaccgtctcaagtacgtcgtccacgttgagcgtgtcacccgtgaca ccatccgaaaggacgacgaggtcaccattgtccgtggttccaacaagggccgcgagggca ctattcgaaaagaagacgaagtaatcatagttcgcggagctttcaagggtagaggaa ttatcatgagcgctcccctctccaaggagctccgcgagcagtacaacgtccgctctattc Conservative 25.0%; 0; Score 102.2; DB : Pred. No. 8.8e-23; Mismatches 118; Indels 366 0; Gaps 357 195 237 255 297 0;

DB 21;

Length

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RESULT 8
AAI52287/c
 04-FEB-2000; 2000US-0180312
26-MAY-2000; 2000US-0207456
                      30-JAN-2001; 2001WO-US00663
                                      09-AUG-2001
                                                     WO200157272-A2
                                                                                   genetic disorder;
                                                                                                       Probe #20973 used to measure gene expression
                                                                                                                        17-OCT-2001
                                                                                                                                       AAI52287;
                                                                                                                                                      AAI52287 standard; DNA; 431
                                                                   sapiens
                                                                                         microarray;
                                                                                                                      (first entry)
                                                                                   SS
                                                                                         human;
                                                                                          placenta;
                                                                                                                                                      ВP
                                                                                          antenatal
                                                                                                        in human placenta
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RESULT
AAF12354
ID AAF1
XX AAF1
XX AAF1
XX AAF1
XX ASPA
XX SASPA
XX Muli
KW Muli
KW ASPA
KW Culi
XX OS ASP
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Best Local
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon analyzing gene expression in huma
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                                      expressed sequence tag; Fusarium venenatum; Aspergillus niger; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recomb culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 431 BP;
                                                                                         Multiple gene expression;
                                                                                                                   Aspergillus
                                                                                                                                             13-MAR-2001
                                                                                                                                                                        AAF12354;
                                                                                                                                                                                                  AAF12354
             Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423
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                                                                                                                                                                                                                                                                                         atacatccatctaatgttgtta 408
                                                                                                                                                                                                                                                                                                                                cggatacatatcgagagagtgaccagagaaaaaagcgaatggaatgactgtacctgtggga
                                                                                                                                                                                                                                                                                                                                                                                                                         CGGCAGAAGTACAATGTCCGCTCCATGCCCATCCGCAAGGACGACGAGGTCCAGGTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCAATGCCCCCTCACACGTGCGCAGGAAGATCATGTCATCCCCGCTCTCCAAGGAGCTG
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                                                                                                                                                                                                                                                                 ATTCACCCAAGCAAGGTGGTTA 102
                                                                                                                                                                                                                                                                                                                    GTCATCTACATCGAGCGGGTGCAGCGTGAGAAGGCCCAACGGCACGACTGTCCACGTGGGC
                                                                                                                                                                                                                                                                                                                                                                       cgcggagctttcaagggtagagaa---ggaaaagttacaacgtgttatcgaaagaaatat
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                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000US-0024263.
                                                                                                                   oryzae
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               oryzae
                                                                                                                                             (first entry)
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                                                                                                                    EST SEQ
                                                                                                                                                                                                  CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; 107 C; 110 G; 139 T; 0 other;
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                                                                                                                                                                                                  747
                                                                                          filamentous fungal cell;
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                                                                                                                    ID NO:4877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                  ВP
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Sequence

747

ВP;

175

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196

G; 166

T; 0 other;

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ce expression of genes in a first filamentous fungal (FF) cell relative to cexpression of the same genes in one or more second filamentous fungal (CC cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The EST'S CC are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the csame genes in one or more second filamentous fungal cells. Monitoring cc same genes in one or more second filamentous fungal cells. Monitoring cc the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be considered, possible functions of unknown open reading frames can be compinized and gene copy number variation and stability can be calculated and gene copy number variation and stability oan be complogenesis, recombination, metabolic pathway poore complogenesis, recombination, metabolic pathway in the production of contabolic pathway in the production of contaboli
                                           engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarray based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Aspergillus ryvae; aAF11854 to AAF11853 represents ESTs from Aspergillus oryvae; and AAF14879 to AAF1875 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monitoring differential expression of uses fluorescence-labeled nucleic aci-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-594572/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for monitoring differential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n of genes in filamentous acids isolated from the c
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Matches 172
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           aggaaaagttacaacgtgttatcgaaagaaatatcggatacatatcgagagagtgaccag
                                                                                                           tttacctattogaaaagaagacgaagtaatcatagttcgcggagctttcaagggtagaga
                                                                                                                                               ccgtgtcatcatgagcgcccctctgagcaaggaactccgtgagaagtacaatgtccgctc
                                                                                                                                                             tttggcctcttcccgccggaagtcgcgcaaggcgcacttcaacgctggctccggcgagcg
                                                                                                                                                                                                            tgtatcgtcgtctagaagaaagcagaggaaagcatactttcaagcaccatcttctgtacg
cgagaagtccaacggccagagcgttcccctcggtatccacccctccaaggtcgtca
                                              gggcaagatcaccagcgtttaccgtcttaagtgggttgtccacgtcgagcgtgtcgtccg
                                                                                               tctccccatccgcaaggacgacgaggtcaccattgtccgtggaggccagaagggccgtga
                                                                                                                                                                                                                                                al Similarity
172; Conser
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                             23.9%; 58.1%;
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                                                                                                                                                                                                                                                            Score 97.6; DB 21
Pred. No. 2.5e-21;
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                    124;
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     373
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RESULT 1
AAH29813
ID AAH2
XX AAH29813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in certain diseases -
          1205
                                                                                                           1145
                                                                                                                                                                                                                 1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1331 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            agttgtatcgtcgtctagaagaaagcagaggaaagcatctttcaagcaccatcttctgt 169
                        agaaggaaaagttacaacgtgttatcgaaagaaatatcggatacatatcgagagagtgac
                                                                                                                                                                                                                                                                                                                                        caaggaaaaggtcaacggtgcttccgttccaattaacttgcacccatccaagcttgtca
                                                                                                agaaggtaagatttcatctgtttacagattgaaatttgccgttcaagttgacaaggttac
                                                                                                                                                                                                    ggccttgccaatcagaagagatgatgaagttttggttgttcgtggttccaagaagggtca 1144
                                                                                                                                                                                                                               ttctttacctattcgaaagaagacgaagtaatcatagttcgcggagctttcaagggtag
                                                                                                                                                                                                                                                                                                          acgtcgtgttttgctatctgctccattatctaaggagttgagagctcaatacggtatcaa
                                                                                                                                                                                                                                                                                                                                                                                                                 agacgtttcctccgacagaaggaaaggctagaaaggcttatttcaccgccccatcctccca 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-367042/38.
DB; AAG70777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fungus; apoptosis; infection; proliferative disease;
e; autoimmune disease; ischaemia; neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-BE00077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99EP-0870141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reekmans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Backer MD,
ekmans RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         associated coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95.8; DB 22;
Pred. No. 1.2e-20;
0; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Luyten WHML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Malcorps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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8 96

atgaagtattccaaagttgtatcgtcgtctagaagaaagcagaggaaggcatactttcaa 155

Conservative

Indels

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Gaps

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atgaagtttaatccctttgtgacttccgaccgaagcaagaatcgcaaaaggcatttcaat 127

Qy 밁

276 188 216 128 156

gctttcaagggtagagaa---ggaaaagttacaacgtgttatcgaaagaaatatcggata

aaatacagcgttcgttctttacctattcgaaaagaagacgaagtaatcatagttcgcgga

aagtacaacgtgcgatccatgcccatccgaaaggatgatgaagttcaggttgtacgtgga

247 275 187

gcaccttcccacattcgaaggaagattatgtcttcccctctttccaaagagctgagacag

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RESULT 1
                Query Match
Best Local
    Matches
                                                                                                  mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                              derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of
                                                                                                                                                                                                                                The present sequence is one of a large number of 5' ESTs derived from RNAs encoding secreted proteins. An ORF has been identified within sequence. The 5' ESTs were prepared from total human RNAs or polyAt
                                                                  Sequence 508
                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 3876; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                diagnostic,
                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                          Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC03878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC03878 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-2000
             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                                                    2000-500381/45
DB; AAG03872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy;
    182;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5' EST;
                                                                                                                                                                                                                                                                                                                forensic,
                                                                  B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; expressed sequence tag;
chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0122487
                                                                 172 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                          J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry
              22.2%;
                                                                                                                                                                                                                                                                                                              gene therapy and chromosome mapping
                                                                 113 C;
                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST,
Score 90.4; DE Pred. No. 4.3e. 0; Mismatches
 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
             90.4; DB :
                                                                 G;
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                                                                                                                                                                                                                                                                                                                                                                                                          Giordano
                                                               100 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3876.
в 21;
-19;
131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; cDNA isolation;
                         Length
                                                                                                                                                                                                                                                                                                               procedures
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RESULT 12
AAF15011
ID AAF150
XX
AAF150
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AAF150
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AAF150
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AF160
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AF160
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AF160
XX
Multi|
KW Multi|

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal (cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS care used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring ct the global expression of genes from FF cells allows the production contential of the microorganisms to be improved. New genes may be considered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be consisted. The expression of genes can be used to study how FF cells campitored. The expression of genes can be used to study how FF cells campitored. The expression of genes can be used to study how FF cells campitored in culture conditions, environmental stress, spore corphogenesis, recombination, metabolic or catabolic pathway cellinearing. Using ESTs provides several advantages over genomic or candon cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the mitroarrays based on function of the gene products to facilitate canditate. AAF11248 to AAF11253 represents ESTs from Aspergillus oryzae; and creaming the constitution of the gene products to facilitate canditate to the constitution of the gene products to facilitate canditate to canditate to AAF11248 to AAF11253 represents ESTs from Aspergillus oryzae; and creaming the constitution of the gene products to facilitate to an expression of the canditate to AAF11248 to AAF11253 represents ESTs from Aspergillus oryzae; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monitoring differential expression of genes uses fluorescence-labeled nucleic acids isol substrate of expressed sequence tags .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200056762-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cactataaaggtcagcaaattggcaaagtagtccaggtttacaggaagaaatatgttatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccatctaatgttgtta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 3043; 3161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rey MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reesei EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enes in filamentous fungal cells isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s,
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                   from Aspergillus
lus oryzae; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olsen
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RRESULT 13
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XX AA1392
XX 17-OCT
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XX Probe
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI39236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI39236 standard; DNA;
                                                                                                            Human genome-derived single exon nucleic acid analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                    04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; microarray; human; placenta; antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe #7922 used to measure gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 58.
nes 169; Conservative
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2000US-0608408.
2000US-0632366.
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2000US-0236359
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                                                                    ID No 7922; 654pp; English.
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  single exon nucleic acid probes (SENP). probe. The probes are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.8;
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4.4e-18;
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present invention relates to present sequence is one such

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; n pathway; promoter; termination sequence; corn: ss.
                                                                                                                                                                                                                                                                                                                                                                              25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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Local Similarity 62.3%;
nes 144; Conservative
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metabolic;
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PR 26-JUL-1999 99US-0145224.
PR 27-JUL-1999 99US-0145915.
PR 27-JUL-1999 99US-0145915.
PR 27-JUL-1999 99US-0145951.
PR 02-AUG-1999 99US-0145368.
PR 02-AUG-1999 99US-0147038.
PR 03-AUG-1999 99US-0147038.
PR 03-AUG-1999 99US-014703.
PR 10-AUG-1999 99US-014793.
PR 11-AUG-1999 99US-014793.
PR 11-AUG-1999 99US-014793.
PR 11-AUG-1999 99US-014793.
PR 11-AUG-1999 99US-014972.
PR 12-AUG-1999 99US-015066.
PR 12-AUG-1999 99US-015066.
PR 13-AUG-1999 99US-015066.
PR 14-AUG-1999 99US-015069.
PR 14-AUG-1999 99US-015
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RESULT 15
AAF11388
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Best Loc
Matches
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25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus niger EST SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-2001
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Monitoring differential expression of gouses fluorescence-labeled nucleic acids substrate of expressed sequence tags -
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                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus niger.
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                                                                                                                                                                    (NOVO ) NOVO NORDISK BIOTECH
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Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atcagtcgccatgaagtattccaaagttgtatcgtcgtctagaagaaagcagaggaaagc 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcacttcacggccccgtcctccgtccgccgcgtgctcatgtccgcggcgctatcgacgga
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146; Conser
                                                                                      2000-594572/56
                                                                                                                                RM,
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                                                                                                                              Rey MW,
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990S-0161404
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990S-0161360
990S-0161361
990S-0161920
990S-0161920
990S-0161923
990S-0161993
990S-0161993
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55.1%;
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                                                                                                                                JR,
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Pred.
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No. 4.
                            genes in filamentous ds isolated from the
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1.3e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for monitoring differential CC expression of genes in a first filamentous fungal (FF) cell relative to CC expression of the same genes in one or more second filamentous fungal CC cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS in a first filamentous fungal (FF) cell relative to expression of genes in a first filamentous fungal (FF) cell relative to expression of the CC same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be consisted and gene copy number variation and stability can be discovered, possible functions of unknown open reading frames can be consisted. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway can complete the consist consistency of the filling filmination of redundancy as one spot on an croatray equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate canalysis of the results. AAF01478 to AAF11247 represents ESTs from Aspergillus organisms of the AAF11854 to AAF11854 represents ESTs from Aspergillus organisms and AAF11879 to AAF1337 represents ESTs from Sporgillus organisms of the presents ESTs from Sporgillus organisms of the presents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.7
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 629 BP; 153 A; 191 C; 155 G; 129 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 87; Page 1742-1743; 3161pp; English.
              250
                                                                                             190 catgcccatccgcaaggacgacgaggtcatggtcgtccgtggcagcaacaagggccgtga
                                                                                                                                                         233
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gggcaaggtcaccagcgtctaccgcctgaagtgggccatccacgtcgagcgcatcagccg
                                aggaaaagttacaacgtgttatcgaaagaaatatcggatacatatcgagagagtgaccag 352
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